

U.S. PTO 88281

09/642218

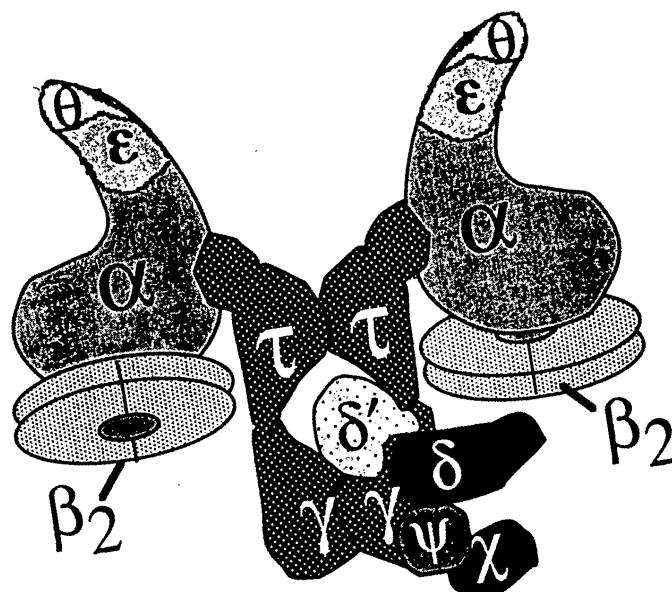


Figure 1

ATP binding

E. coli

MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAK

B. subtilis

MSYQALYRVFRPQRFEDVVGQEHITKTLQNALLOKKFSSHAYLFSGPRGTGKTSAAKIFAK

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E. coli

GLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRF

B. subtilis

AVNCEHAPVDEPCNECAACKGITNGSISDVIEIDAASNNGVDEIRDIRDKVKFAPSAVTY

. *** . * * . * . * . * . * * * * * . * . . * * . * * . * * . . .

E. coli

KVYLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATTPQKLPVTILSRCLQFHLKALDV

B. subtilis

KVYIIDEVHMLSIGAFNALLKTLEEPPEHCIFILATTEPHKIPLTIISRCQRFDFKRITS

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Figure 2

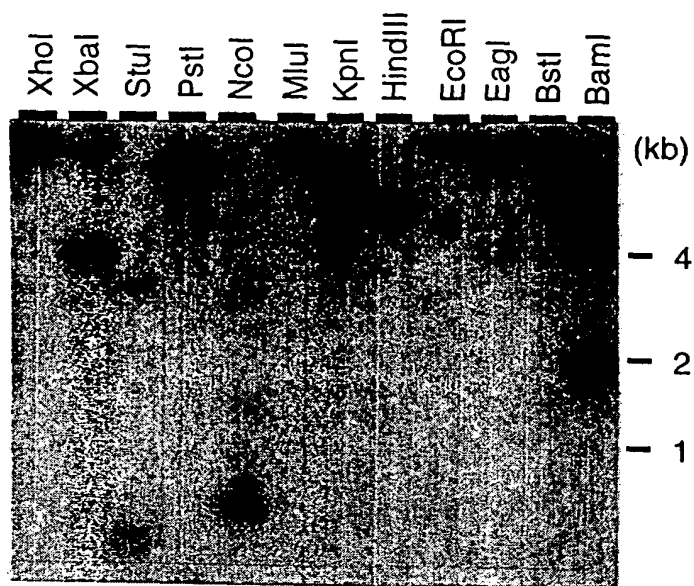


Figure 3

600-1-179 N (Sheet 4 of 31)

TCCGGGGGTG	GGGTTCCCAG	GTAGACCCCG	GCCCCTCCCG	TGAGCCCCTT	TACCCAGGCC	60
GCCACCTCCT	CCAGGGGGGC	CAAGGCGTGC	AAGGAGAGGA	ACGTCCGCAC	CACGCCCTAT	120
					S.D.	
ACTAGCCTT	GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG	met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val	180			(17)
					CAC	
GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG	gly gln glu his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln	240				(37)
GCS TAC CTS TTC TCC GGS AC						
GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC	ala tyr leu phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala	300				(57)
ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG	met ala val gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala	360				(77)
GtG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCC AGC AAC AAC TCC GTG	Val gln arg gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val	420				(97)
GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG	glu asp val arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys	480				(117)
					C	
GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG	Val phe ile leu asp Glu ala his met leu ser lys ser ala phe asn ala leu leu lys	540				(137)
TGS CTS CTC CTC GGS GGS CTC GTG						
ACC CTG GAG GAG CCC CCG CCC CAC GTC CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG	Lhr leu glu glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg	600				(157)
ATG CCC CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CGC CTC ACG GAG GAG	met pro pro thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu	660				(177)
GAG ATC GCC TTT AAG CTC CGG CGC ATC CTG GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG	glu ile ala phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu	720				(197)
GCC CTC CTC CTC CTC GCC CGC CTG GCG GAC GGG GCC CTT AGG GAC GCG GAA AGC CTC CTG	ala leu leu leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu	780				(217)
GAG CGC TTC CTC CTC CTG GAA GGC CCC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC	glu arg phe leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly	840				(237)
TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCC TCC CTC GCG AGG GGG AAA ACG GCG	ser pro pro gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala	900				(257)
GAG GCC CTG GGC CTC GCC CGG CGC CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTG GTC	glu ala leu gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val	960				(277)
TCG GGC CTT TTG GAG GTG TTC CGG GAA GGC CTC TAC GCC GCC TTC GGC CTC GCG GGA ACC	ser gly leu leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr	1020				(297)
CCC CTT CCC GCC CCG CCC CAG GCC CTG ATC GCC GCC ATG ACC GCC CTG GAC GAG GCC ATG	pro leu pro ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met	1080				(317)

Figure 4A

GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA	1140
glu arg leu ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly	(337)
AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC	1200
arg ala leu ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly	(357)
CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG	1260
pro lys pro glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu	(377)
CGG GAG CGG TGG CGG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CGG	1320
arg glu arg trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg	(397)
GAG GCC CGC CCG GAG GTC CGG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC	1380
glu ala arg pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala	(417)
TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT	1440
phe his tyr arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his	(437)
frameshift site	
TTC GGG GTG GAG GAG GTC GTC CTC GTC CTG GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG	1500
phe gly val glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg	(457)
CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA	1560
pro arg pro ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val	(477)
GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CGG GTG GTC CGC CTC	1620
glu ala glu glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu	(497)
CTG GGG GGG CGG GTG CTC TGG GTG CGG CGG CCC AGG ACC CGG GAG GCG CCG GAG GAG GAA	1680
leu gly gly arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu	(517)
CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA TGGGGGCATG ACGCGGACCAC	1740
pro leu ser gln asp glu ile gly gly thr gly ile *	(529)
CGACCTCGGA CAAGAGACCG TGGACAACAT CCTCAAGCGC CTCCGCCGTA TTGAGGGCCA	1820
GGTGCGGGGG CTCCAGAAGA TGGTGGCCGA GGGCCGCCCC TGCACGAGG TCCTCACCAC	1880
GATGACCGCC ACCAAGAAGG CCATGGAGGC GGCGGCCACC CTGATCCTCC ACGAGTTCCT	1940
GAACGTCTGC GCCGCCGAGG TCTCCGAGGG CAAGGTGAAC CCCAAGAAGC CCGAGGAGAT	2000
CGCCACCATG CTGAAGAACT TCATCTA	2027

Figure 4B

GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG 51
 GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG 111
 GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC 171
 ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG 231
 GTG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCC AGC AAC AAC TCC GTG 291
 GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG 351
 GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG 411
 ACC CTG GAG GAG CCC CCG CCC CAC GTC CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG 471
 ATG CCC CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CGC CTC ACG GAG GAG 531
 GAG ATC GCC TTT AAG CTC CGG CGC ATC CTG GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG 591
 GCC CTC CTC CTC CTC GCC CGC CTG GCG GAC GGG GCC CTT AGG GAC GCG GAA AGC CTC CTG 651
 GAG CGC TTC CTC CTC CTG GAA GGC CCC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC 711
 TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCC TCC CTC GCG AGG GGG AAA ACG GCG 771
 GAG GCC CTG GGC CTC GCC CGG CGC CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTG GTC 831
 TCG GGC CTT TTG GAG GTG TTC CGG GAA GGC CTC TAC GCC GCC TTC GGC CTC GCG GGA ACC 891
 CCC CTT CCC GCC CCG CCC CAG GCC CTG ATC GCC GCC ATG ACC GCC CTG GAC GAG GCC ATG 951
 GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA 1011
 AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC 1071
 CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG 1131
 CGG GAG CGG TGG CGG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CGG 1191
 GAG GCC CGC CCG GAG GTC CGG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC 1251
 TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT 1311
 TTC GGG GTG GAG GAG GTC GTC CTC GTC CTG GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG 1371
 CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA 1431
 GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CGG GTG GTC CGC CTC 1491
 CTG GGG GGG CGG GTG CTC TGG GTG CGG CGG CCC AGG ACC CGG GAG GCG CCG GAG GAG GAA 1551
 CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA (1590)

Figure 4C

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
 his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
 phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
 gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
 gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
 arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
 leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
 glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
 thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
 phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu ala leu leu 200
 leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
 leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
 gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
 gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
 leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
 ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
 ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
 ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
 glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
 trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
 pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
 arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
 glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg pro arg pro 460
 ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val glu ala glu 480
 glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu leu gly gly 500
 arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu pro leu ser 520
 gln asp glu ile gly gly thr gly ile 529

Figure 4D

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Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
glu glu val val leu val leu glu gly glu lys lys lys pro asp pro lys ala pro pro 460
gly pro thr ser 464

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Figure 4E

Met	ser	ala	leu	tyr	arg	arg	phe	arg	pro	leu	thr	phe	gln	glu	val	val	gly	gln	glu	20
his	val	lys	glu	pro	leu	leu	lys	ala	ile	arg	glu	gly	arg	leu	ala	gln	ala	tyr	leu	40
phe	ser	gly	pro	arg	gly	val	gly	lys	thr	thr	thr	ala	arg	leu	leu	ala	met	ala	val	60
gly	cys	gln	gly	glu	asp	pro	pro	cys	gly	val	cys	pro	his	cys	gln	ala	val	gln	arg	80
gly	ala	his	pro	asp	val	val	asp	ile	asp	ala	ala	ser	asn	asn	ser	val	glu	asp	val	100
arg	glu	leu	arg	glu	arg	ile	his	leu	ala	pro	leu	ser	ala	pro	arg	lys	val	phe	ile	120
leu	asp	glu	ala	his	met	leu	ser	lys	ser	ala	phe	asn	ala	leu	leu	lys	thr	leu	glu	140
glu	pro	pro	pro	his	val	leu	phe	val	phe	ala	thr	thr	glu	pro	glu	arg	met	pro	pro	160
thr	ile	leu	ser	arg	thr	gln	his	phe	arg	phe	arg	arg	leu	thr	glu	glu	glu	ile	ala	180
phe	lys	leu	arg	arg	ile	leu	glu	ala	val	gly	arg	glu	ala	glu	glu	glu	ala	leu	leu	200
leu	leu	ala	arg	leu	ala	asp	gly	ala	leu	arg	asp	ala	glu	ser	leu	leu	glu	arg	phe	220
leu	leu	leu	glu	gly	pro	leu	thr	arg	lys	glu	val	glu	arg	ala	leu	gly	ser	pro	pro	240
gly	thr	gly	val	ala	glu	ile	ala	ala	ser	leu	ala	arg	gly	lys	thr	ala	glu	ala	leu	260
gly	leu	ala	arg	arg	leu	tyr	gly	glu	gly	tyr	ala	pro	arg	ser	leu	val	ser	gly	leu	280
leu	glu	val	phe	arg	glu	gly	leu	tyr	ala	ala	phe	gly	leu	ala	gly	thr	pro	leu	pro	300
ala	pro	pro	gln	ala	leu	ile	ala	ala	met	thr	ala	leu	asp	glu	ala	met	glu	arg	leu	320
ala	arg	arg	ser	asp	ala	leu	ser	leu	glu	val	ala	leu	leu	glu	ala	gly	arg	ala	leu	340
ala	ala	glu	ala	leu	pro	gln	pro	thr	gly	ala	pro	ser	pro	glu	val	gly	pro	lys	pro	360
glu	ser	pro	pro	thr	pro	glu	pro	pro	arg	pro	glu	glu	ala	pro	asp	leu	arg	glu	arg	380
trp	arg	ala	phe	leu	glu	ala	leu	arg	pro	thr	leu	arg	ala	phe	val	arg	glu	ala	arg	400
pro	glu	val	arg	glu	gly	gln	leu	cys	leu	ala	phe	pro	glu	asp	lys	ala	phe	his	tyr	420
arg	lys	ala	ser	glu	gln	lys	val	arg	leu	leu	pro	leu	ala	gln	ala	his	phe	gly	val	440
glu	glu	val	val	leu	val	leu	glu	gly	glu	lys	lys	lys	ala							454

Figure 4F

		ATP site	
E.coli	MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAK		60
H.inf.K.....II.....KDN.L.....F..		60
B.sub.A.Y.VF...R.E.....ITKT.Q.A.LQKKFS.....P..T....A.KIF..		60
C.cres.	DA.T.....Y..R..E.LI...AMVRT...AF.T...A..FMLT.V.....TT.....R		113
M.gen.	-MH..FYQ.Y..IN.KQTL...SIRKI.V.AINRDKLPNG.I...E..T...TF.KII..		59
T.th.	--VSA.Y.RF..L..QE.....KEP.LKAIRE..LAQ.....P.....TT.....M		58
		Zn ⁺⁺ finger	
		* * *	
E.coli	GLNCET---GITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPA		116
H.inf.	...VH---.V.....E.E..KA....N.I.....E.....K.V		116
B.sub.	AV...H---APVDE..NE.AA.KG.TN.SIS.V.....NNG.DEI..IR.K.KF..S		116
C.cres.	A..Y..DTVK.PSVDLTTEGYH..S.IE..HM.VL.L.....DEM.E...G.R...V		173
M.gen.	AI..LN---WDQIDV.NS..V.KS.NTNSAI.IV.....KNGIN.I.E.VE..FNH.F		115
T.th.	AVG.QG-----EDP.....PH.QAVQR.AHP.VVD.....NNS...V.E.RERHL..L		112
E.coli	RGRFKVYLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATDPQKLPVTILSRCLQFHLK		176
H.inf.	V.....Y.....		176
B.sub.	AVTY...I.....IGA.....CI.I....E.H.I.L..I..QR.DF.		176
C.cres.	EA.Y...I.....TAA.....P.A..IF...EIR.V.....QR.D.R		233
M.gen.	TFKK...IL..A...TTQ.WGG.....S.PY.L.IFT..EFN.I.L.....QS.FF.		175
T.th.	SAPR..FIL..A...KSA.....P..L.VF...E.ERM.P.....TQH.RFR		172
E.coli	ALDVEQIRHQLEHILNEEHIAHEPRALQLLARAAEGSLRDALSLTDQAIASGDGQ--VST		234
H.inf.	...ET..SQH.A...TQ.N.PF.DP..VK..K..Q..I..S.....M..R.--.TN		234
B.sub.	RITSQA.VGRMNK.VDA.QLQV.EGS.EII.S..H.GM.....L....SFSGDI--LKV		234
C.cres.	RVEPDVLVKHFDR.SAK.GARI.MD..A.I.....V..G...L...VQTERGQT.TS		293
M.gen.	KITSDL.LER.ND.AKK.K.KI.KD..IKI.DLSQ.....G...L..LAI.LIVKKL.LL		235
T.th.	R.TE.E.AFK.RR..EAVGREA.EE..L...L.D.A...E..LERFLLLEGP---LTR		229
E.coli	QAVSAMLGTLDDDDQALSLVEAMVEANGERVMA LINEAAARGIEWEALLVEMLGLLHRIAM		294
H.inf.	NV..N...L...NYSVDILY.LHQG...LL.RTLQRV.DAAGD.DK..G.CAEK..Q..L		294
B.sub.	EDALLIT.AVSQLYIGK.AKSLHDK.VSDALETL..LLQQ.KDPAK.IED.IFYFRDMLL		294
C.cres.	TV.RD...LA.RS.TIA.Y.HVMAGKTKDALEGFRALWGF.ADPVVMLDV.DHC.AS.V		353
M.gen.	MLKKHLISLIEMQNL.L.KQFYQ.I		260
T.th.	KE.ERA..SPPGTGVAEIAASLARGKTAEALG.ARRLYGE.YAPRS.VSGL.EVFREGLY		289

Figure 5



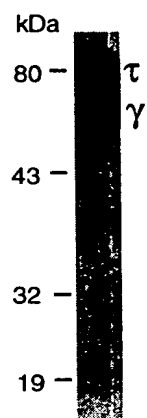
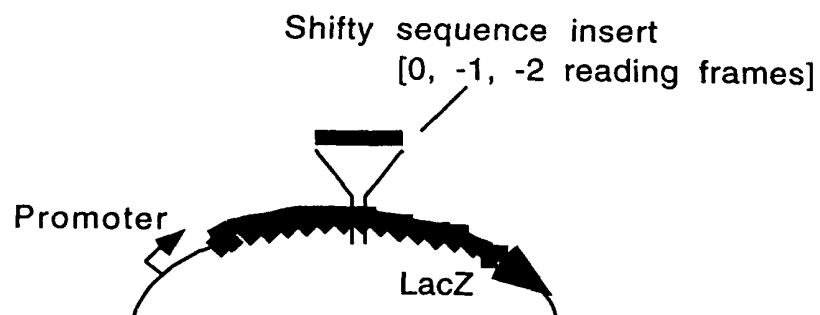


Figure 7



	Reading frame	Blue	White
Shifty sequence	0	+	
	- 1	+	
	- 2	+	
Mutant sequence	0	++	
	- 1		+
	- 2		+

Figure 8

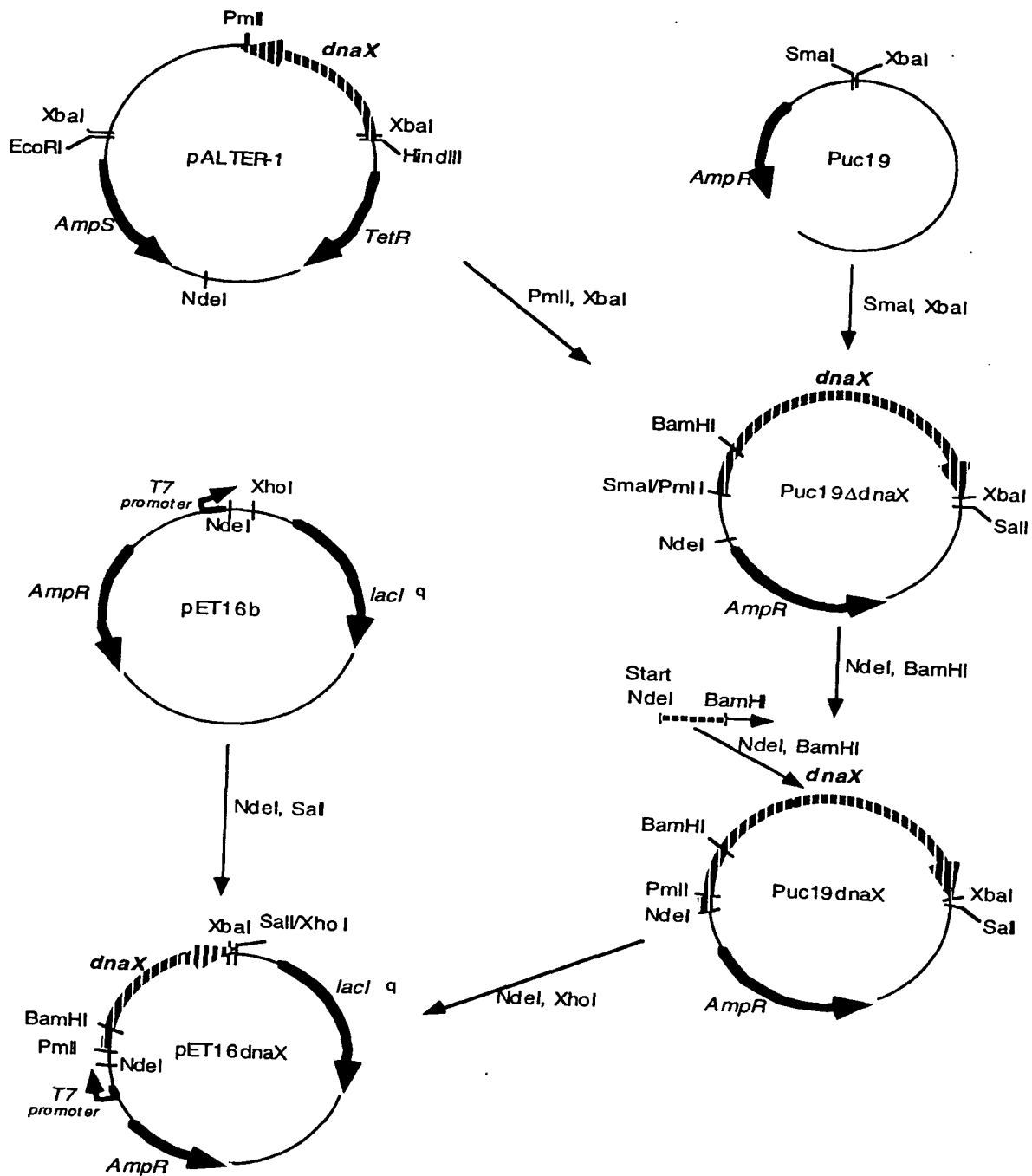


Figure 9

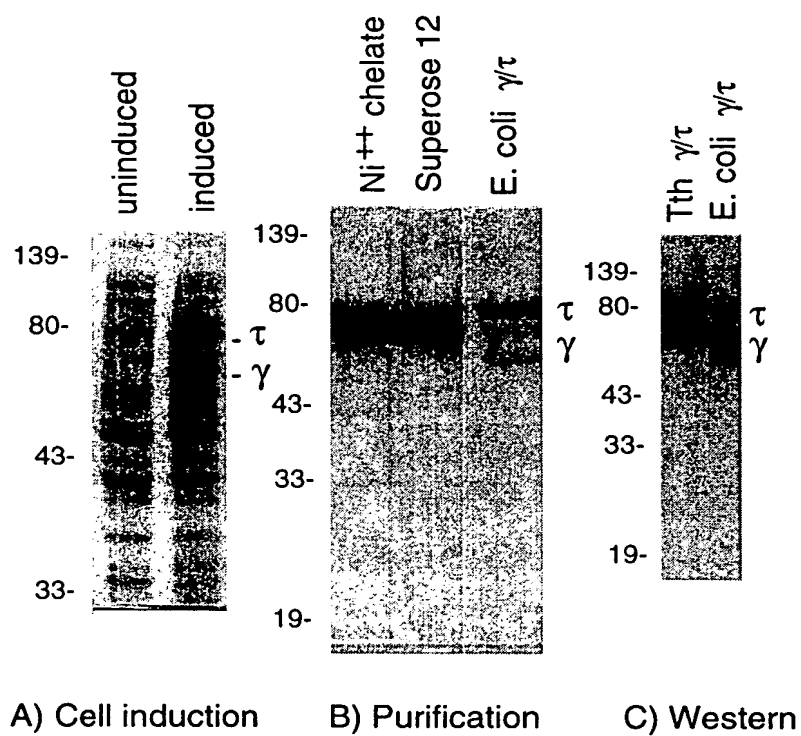


Figure 10

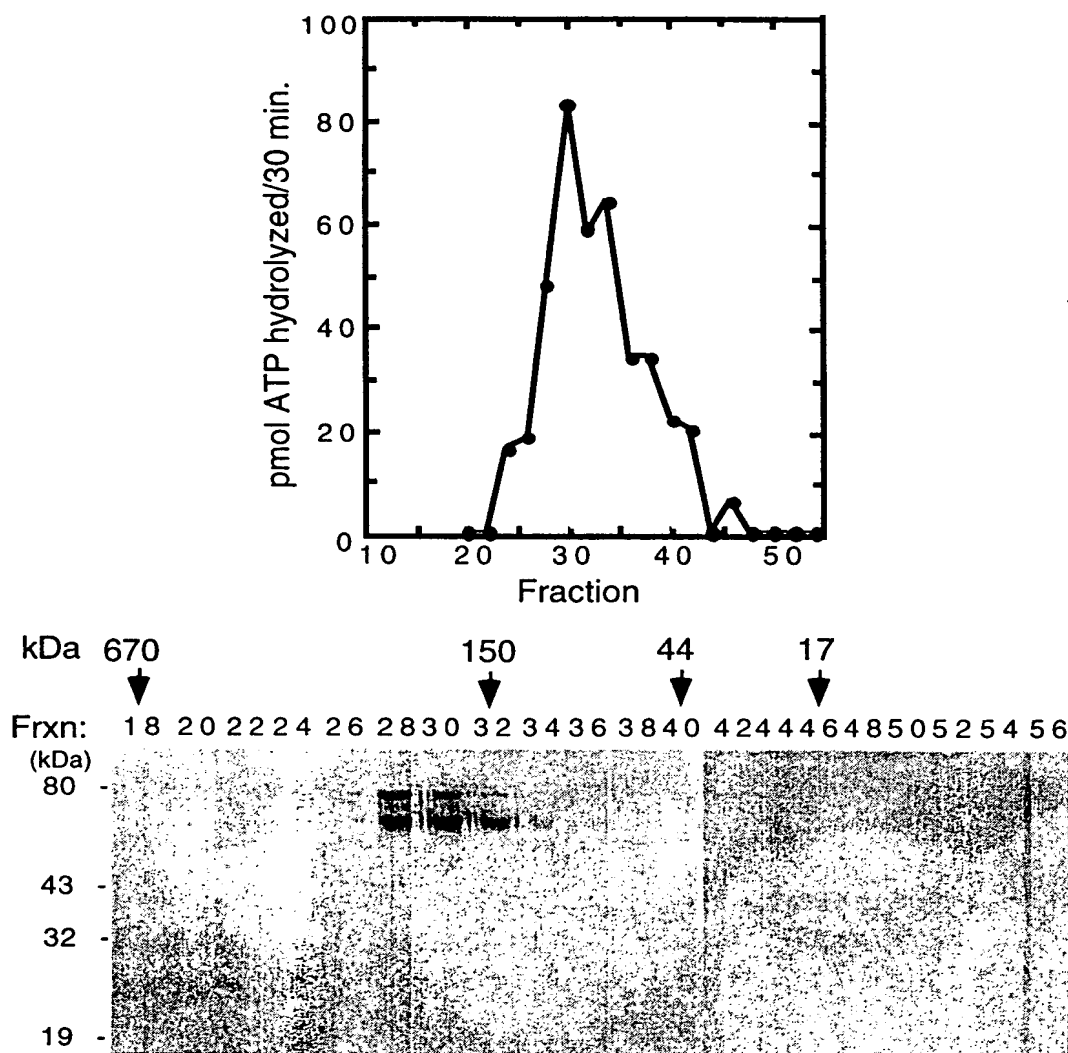


Figure 11

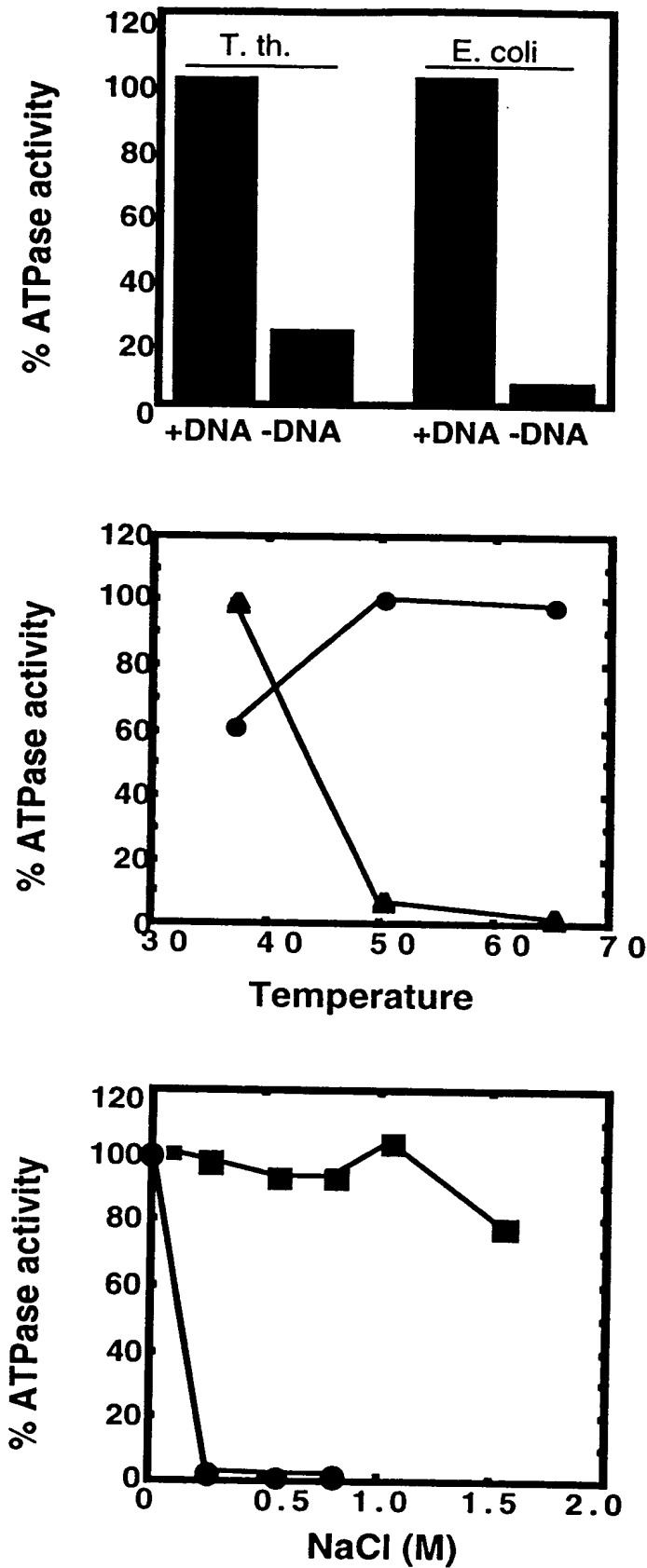
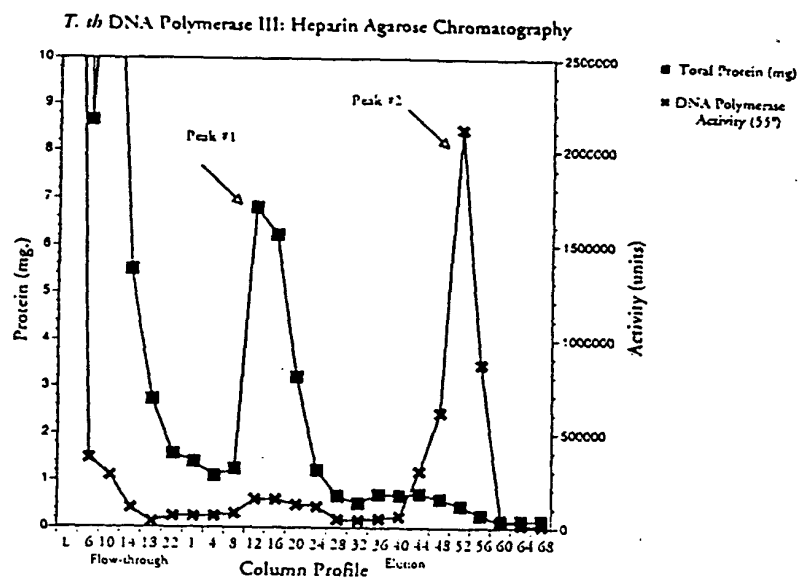


Figure 12

A)



B) ATP Agarose Step Column

C)

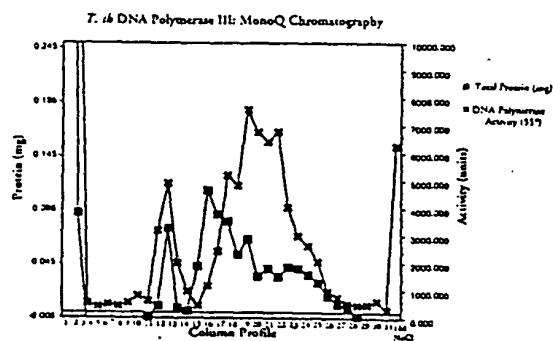
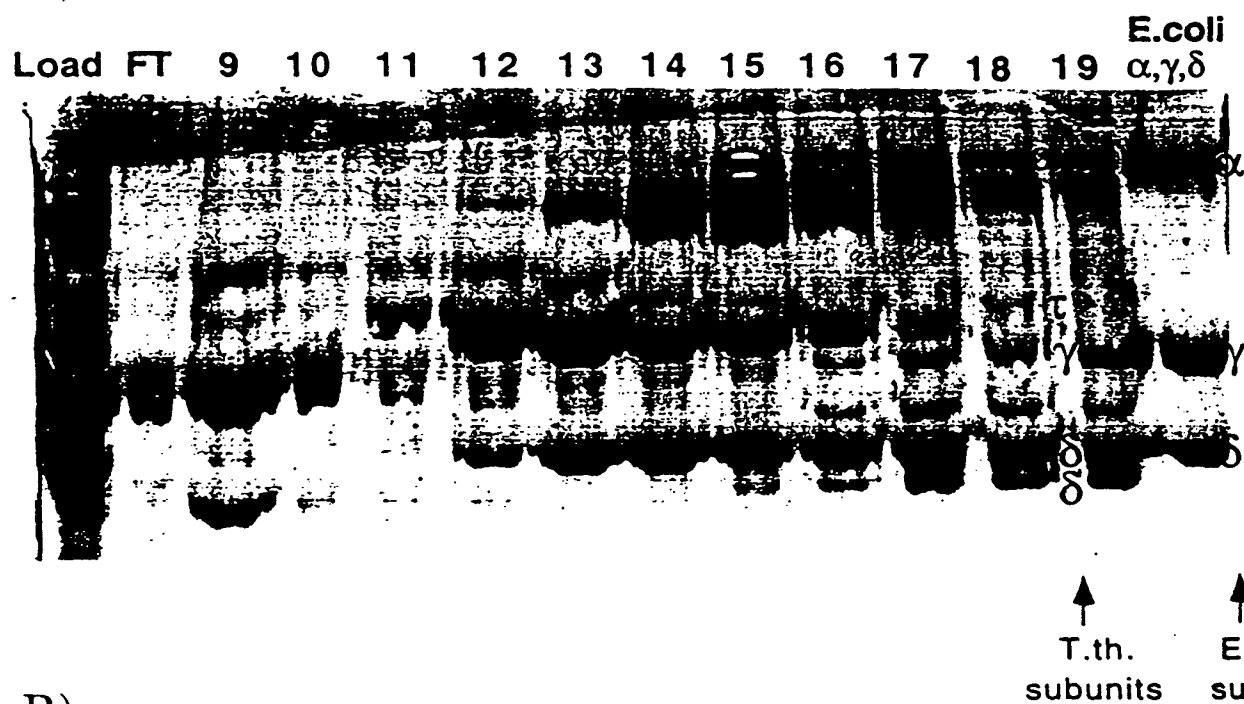


Figure 13

A)



B)

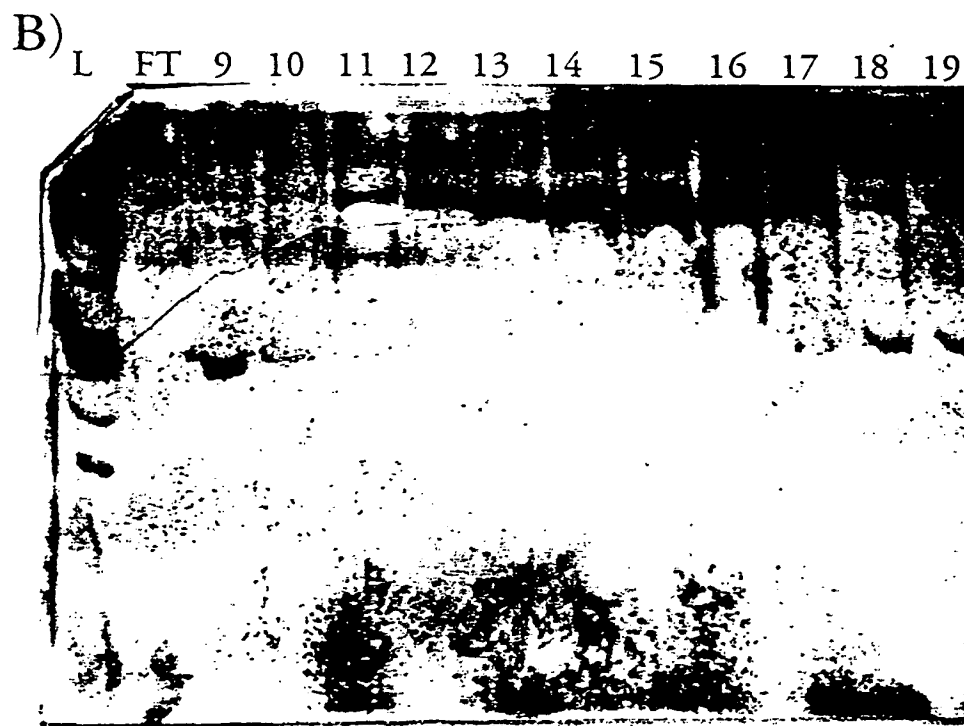


Figure 14

A) Alignment of TTH1 with alphas subunits of other organisms.

E.coli	DRYFLELIRTGRPDEESYLHAAVELAEARGLPVV	197	(ID#72)
V.chol.	DHFYLELIRTGRADEESYLHFALDVAEQYDLPVV	197	(ID#73)
H.inf.	DHFYLALSRTGRPNEERYIQAALKLAERCDLPLV	197	(ID#74)
R.prow.	DRFYFEIMRHDLPPEEQFIENSYIQIASELSIPIV	195	(ID#75)
H.pyl.	DDFYLEIMRHGILDQRFIDEQVIKMSLETGLKII	213	(ID#76)
S.sp.	DDYYLEIQDHGSVEDRLVNINLVKIAQELDIKIV	202	(ID#77)
M.tub.	DNYFLELMDHGLTIERRVRDGLLEIGRALNIPPL	220	(ID#78)
T.th.	FFIEIQNHGLSEQK		(ID#61)

B) Alignment of TTH2 with alphas subunits of other organisms.

E.coli	NKRRAKNGEPPLDIAAIPDDKKSFDMLQRSETTAVFQLESRGMKD	618	(ID#79)
V.chol.	NPRLKKAGKPPVRIEAIPLDDARSFRNLQDAKTTAVFQLESRGMKE	618	(ID#80)
H.inf.	NVRMVREGKPRVDIAAIPDDPESFELLKRSETTAVFQLESRGMKD	618	(ID#81)
R.prow.	CKKLLKEQGIKIDFDDMTFDDKKTQMLCKGKGVGVFQFESIGMKD	624	(ID#82)
H.pyl.	LKIIKTQHKISVDFLSLDMDDPKVYKTIQSGDTVGIQFQIES-GMFQ	648	(ID#83)
S.sp.	QERKALQIRARTGSKKL PDDVKKTHKLEAGDLEGIFQLESQGMKQ	643	(ID#84)
M.tub.	IDNVRANRGIDLDESVPDDKATYELLGRGDTLGVFQLDGGPMRD	646	(ID#85)
T.th.	RVELDYDALTLDD		(ID#60)

Figure 15

A)

Start codon

ATGGGCGGGGAGCTCCGCTTCGCCCACCTCCACCAGCACA
CCCAGTTCTCCCTCCTGGACGGGGCGCCGAAGCTTTCCGA
CCTCCTCAAGTGGGTGGAGGAGACGACCCCGAGGACCCC 120
GCCTTGGCCATGACCGACCACGGCAACCTCTTCGGGGCCG
TAGAGTTCTACAAGAAGGCCGCCGAAATGGGCATCGAGCC
CATCCTGGGTACGAGGCCTTACGTGGCGGCGGAAAGCCCG 240
TTTGACCGCAAGCGGGGAAAGGGCCTAGACGGGGGCTACT
TTCACCTCACCTCCTCGCCAAGGACTTCACGGGGTACCA
GAACCTGGTGCGCCTGGCGAGCCGGGCTTACCTGGAGGGG 360
TTTTACGAAAAGCCCCGGATTGACCGGGAGATCCTGCGCG
AGCGCCGAGGGCCTCATCGCCTCTCGGGGTGCCTCGGGGC
GGAGATCCCCCAGTTTCATCCTCCAGGACCGTCTGGACCTG 480
GCCGAGGCCCCGGCTCAACGAGGACCTCTCCATCTTCAAGG
ACCGCTTCTTCATTCACATCCAGAACCACGGCCTCCCCGA
GCAGAAAAAGTCAACGAGGTCCCTCAAGGAGTTCGCCCCG 600
AAGTACGGCCTGGGGATGGTGGCCACCAACGACGGCCATT
ACGGGAGGAAGGAGGCCCCGACGCGCCACGAGGTTTTCCT
CGCCATCCAGTCCAAGAGCACCTTGGACGACCCCGGGGCC 720
GTTGGCTTTCCCCTGCGGGAGTTCTACGTGAAGACCCCCG
AGGAGACGTGCGGGCCGGTGTTCCTCCGAGGAGGAGTGGGG
GGACGAGCCCTTTGACAACACCGTGGAGATCGCCCGCATG 840
TGCAACGTGGAGCTGCCCATCGGGACAAGATGGTCTACCC
GAATCCCCCGCTTCCCCCTCCCCGAGGGACCGGGGACCGA
GGCCAAGTACCTAATGGAGCTAACCTTCAAGGGGGCCCTC 960
CGCCGTTACCCGGACCGAATCACCGAGGGTTTCTACCGGG
AGGTTTTCGCGCCTTTTGGGGAAGCTTCCCCCCCACGGGCA
CGGGGAGGCCTTGGCCGAGGCCTTGGCCCAGGTGGAGCGG 1080
GAGGCTTGGGAGAGGCTCATGAAGAGCCTCCCCCCTTG
ACCGGGTCCAAGGAGTTCCA

B)

MGRELRF AHLHQHTQFSLLDGAPKLSDLLKWVEETTPEDP
ALAMTDHGNLFGAVEFYKKAEMGIEPILGTRPYVAAESP
FDRKRKGKLDGGYFHLTLAKDFTGYQNLVRLASRAYLEG 120
FYEKPRIDREILRERRGPHRLSGCLGAEIPQFILQDRLDL
FFIEIQNHGLSEQK
AEARLNEDLSIFKDRFFIHIQNHGLPEQKKVNEVLKEFAR
KYGLGMVATNDGHYGRKEARSAHEVFLAIQSKSTLDDPGA 240
VGFPLREFYVKTPREETCGPVFP EE EWGDEPFDNTVEIARM
CNVELPIGTRWSTRI PRFPLPEGPGTEAKYLMELTFKGPL
RRYPDRITEGFYREVFRLLGKLPPHGHGEALAEALAQVER 360
EAWERLMKSLPPFDRGPRSS

Figure 16

	Start1	Start2	3'-Exo I
T.th.	VERVVRTLLDGRFLLEEGVGLWEWRYPPFLEGEAVVVLDLETTGLAG-----		LDEVIEVGLLRLEGG---RRLPF
D.rad.			PWPQDVVVFDLETTGFSPA-----SAAIVEIGAVRIVGGQIDETLKF
Bac.sub.	HGIKMIYGMEANLVDDGVPIAYNAHRLLEEET	YVVFDVETTGLSAV-----	YDTIIELA AVKVKGGE--IIDKF
H.inf.			MINPNRQIVLDTETTGMNQLGAHYEGHCHIEIGAVELINRR-YTGNNX
E.c.			MSTAITRQIVLDTETTGMNQIGAHSEGHKIIIEIGAVEVNNRR-LTGNNF
H.pyl.	NLEYLKACGLNFIETSENLITLKNLKTPLKDEV	FSFIDLETTGSCPI-----	KHEILEIGAVQVKGGE--IINRF

			3'-Exo II
T.th.	QSLVR-PLPP---AEARSWNLT--GIPREALEEAPSLEEVLKAYPLRGDATLVIHNAAFDLGFL-RPALEGLG		
D.rad.	ETLVR-PTRPDGSMLSIPWQAQRVHGISEMVRRAPAXKDVLPDFDFVDGSAVVAHNVSFDGGFM-RAGAERLG		
Bac.sub.	EAFAN-PHRP---LSATIIELT--GITDDMLQDAPDVVDVIRDFREWIGDDILVAHNASFDMGFL-NVAYKKLL		
H.inf.	HIYIK-PDRP---XDPDAIKVH--GITDEMLADKPEFKEVAQDFLDYINGAELLIHNAFPDVGFM-DYEFKRLN		
E.c.	HVYLK-DRLV---DPEAFGVH--GIAVDFLDKPTFAEVAVEFMDYIRGAELVIHNAAFDIGFM-DYEFSLK		
H.pyl.	ETLVKVKVSP-----DYIAELT--GITYEDTLNAPSAHEALQELRLFLGNSVVFVAHNANFDYNFLGRYFVEKLH		

		3'-Exo IIIC
T.th.	-----YRLNPVVDLSRLARRGLPGLRRYGLDALSEVLELPRRT--CHRALEDVERTLAVVHEVYYMLT-----SG	
D.rad.	----LSWAPERELCTMQLSRRAFP RERTHNLTVLAERLGLFAPGGRHRSYGDVQVTAQAYLRLLLELLG-----ER	
Bac.sub.	E---VEKAKNPVIDTLELGRFLYPEFKNHRNLTLCKKFDIELTQ--HHRAIYDTEATAYLLLKMLKDAA-----EK	
H.inf.	-LNVKTDDICLVTDTLQMARQMPGKRN-NLDALCDRLGIDNSKRTLHGALLDAEILADVYLMMTGGQTNLFDEEE	
E.c.	RDIAKTNTFCVTDLSLAVARKMFPKGKRN-SLDALCARYEIDNSKRTLHGALLDAQILA EVYLAMTGGQTSMAFAME	
H.pyl.	-----CPLLNLKLC TLDLSKRAILSMRY-SLSFLKELLGFGIEV--SHRAYADALASYKLFEICLLNLP--SYIKT	

Figure 17

A)

ATGGTGGAGCGGGTGGTGCGGACCCCTTCTGGACGGGAGGT 40
 TCCTCCTGGAGGAGGGGGTGGGGCTTTGGGAGTGGCGCTA
 CCCCTTTCCCCTGGAGGGGGAGGCGGTGGTGGTCTCTGGAC 120
 CTGGAGACCACGGGGCTTGCCGGCCTGGACGAGGTGATTG
 AGGTGGGCCTCCTCCGCCTGGAGGGGGGGAGGCGCCTCCC 200
 CTTCAGAGCCTCGTCCGGCCCCCTCCCCGCCCGCCGAAGCC
 CGTTCGTGGAACCTCACCGGCATCCCCGGGAGGCCCTGG 280
 AGGAGGCCCCCTCCCCTGGAGGAGGTTCTGGAGAAGGCCTA
 CCCCCTCGCGGCGACGCCACCTTGGTGATCCACAACGCC 360
 GCCTTTGACCTGGGCTTCTCCGCCCGGCCTTGGAGGGCC
 TGGGCTACCGCCTGGAAAACCCCGTGGTGGACTCCCTGCG 440
 CTTGGCCAGACGGGGCTTACCAGGCCTTAGGCGCTACGGC
 CTGGACGCCCTCTCCGAGGTCCTGGAGCTTCCCCGAAGGA 520
 CCTGCCACCGGGCCCTCGAGGACGTGGAGCGCACCCCTCGC
 CGTGGTGCACGAGGTATACTATATGCTTACGTCCGGCCGT 600
 CCCCACGCTTTGGGAACTCGGGAGGTAG

B)

MVERVVRTLDDGRFLLEEGVGLWEWRYPPFLEGEAVVVD 40
 LETTGLAGLDEVIEVGLLRLEGGRRLPFQSLVRPLPPAEA
 RSWNLGTIPREALEEAPSLEEVLEKAYPLRGDATHVIHNA 120
 AFDLGLFLRPALEGLGYRLENPVVDSLRLARRGLPGLRRYG
 LDALSEVLELPRRTCHRALEDVERTLAVVHEVYYMLTSGR 200
 PRTLWELGRZ

Figure 18

Alignment of dnaA genes.

P.mar.	MLEASWEK	VQSSL--KQNLK--	-----PSYE	TWIRPTEFSG--FKN	GELTLIAPNSFSSAW	LKNYSQTIQETAE-	65
Syn.sp.	MVSCENLWQQ	ALAIL--ATQLTK--	-----PAFD	TWIKASVLIS--LGD	GVATIQVENGFLNH	LQKSYGPLLMEVLT-	67
B.sut.	MENILDLWNQ	ALAQI--EKKLSK--	-----PSFE	TWMKSTKAHS--LQG	DTLTITAPNEFARDW	LESRYLHLIADTIY-	67
M.tub.	MTDDPGSGFTTVWNA	VVSELNGDPKVDDGP	SSDANLSAPLTPQQR	AWLNLVQPLT--IVE	GFALLSVPSFVQNE	IERHLRAPITDALS-	87
T.th.	MSHEAVWQH	VLEHI--RRSITE--	-----VEFH	TWFERIRPLG--IRD	GVLELAVPTSFALDW	IRRHVAGLIQEGPR-	66
E.coli	MSLSLWQQ	CLARL--QDELP--	-----TEFS	MWIRPLQAE--LSD	NTLALYAPNRFVLWD	VRDKYLNNINGLLT-	64
T.mar.	MKER	ILQEI--KTRVNR--	-----KSWE	LWFSSFDVKS--IEG	NKVVSFVGNLFIKEW	LEKKYYSVLKSAVK-	61
H.pyl.	MDTNNNIEKE	ILALVKQNPKVS-	-----IEYE	NYFSQLKYNPNASKS	DIAFFYAPNQVLCTT	ITAKYGALLKEILSQ	72
P.mar.	EIFG---EPVTVHVK	VKANAESSDEHYSSA	P-----	---ITPPLEASPGSV	DSSGSSLRLSK----	-KTLPLNLRYVFN	130
Syn.sp.	DLTG---QEITVKLI	TDGLEPHS---LIGQ	E-----	---SSLPMETTP----	-----	-KNATALNGKYTF	115
B.sut.	ELTG---EELSIKFI	IPQNQDVEDFMPKPQ	VKKAVKEDTSDFPQN	-----	-----	-----MLNPKYTF	119
M.tub.	RRLGH-QIQLGVRIA	PPATDEADDTTVPPS	ENPATSPDITTDND	EIDDSAAARGDNQHS	WPSYFTERPHNTDSA	TAGVTSLNRRYTF	176
T.th.	LLGAQ-APRFELRVV	PGVVVEDIDFQPPPS	PPAQAPQ-	-----	-----	-----EDTFKT	108
E.coli	SFCGADAPQLRFEVG	TKPVTQTPOAAVTSN	VAAPAQVAQTQPORA	APSTRSGWDNVPAPA	EP-----	-TYRSNVNVKHTF	140
T.mar.	VVLG---NDATFEIT	YEAPEPHSSYSEPLV	KKRAVLLTP----	-----	-----	-----LNPDYTFE	106
H.pyl.	NKVG-MHLAHSVDVR	IEVAPKIQINAQSN	NYKAIKTS-----	-----	-----	-----VKDSYTFE	118
P.mar.	FVVGPNSRMAHAAAM	AVAESPGREFNPLFI	CGGVGLGKTHLMQAI	GHYRLEIDPGAKVSY	VSTETFTNDLIL--A	IRQDRMQAFDRYR-	217
Syn.sp.	FVVGPTNRMAHAASL	AVAESPGREFNPLFL	CGGVGLGKTHLMQAI	AHYRLEMYPNAKVY	VSTERFTNDLIT--A	IRQDNMEDFRSYR-	202
B.sut.	FVIGSGNRFABAASL	AVAEPAPAKAYNPLFI	YGGVGLGKTHLMHAI	GHYVIDHNPSAKVVY	LSSEKFTNEFIN--S	IRDNKAVDFRNRYR-	206
M.tub.	FVIGASNRFABAAL	AIAEAPARAYNPLFI	WGESGLGKTHLLHAA	GNVYQRLFPQMRVKY	VSTEEFTNDFIN--S	LRDDRKVAFKRSYR-	263
T.th.	SWWGPTTPWPHGGAV	AVAESPGRAYNPLFI	YGGRGLGKTYLMAHV	GPLRAKRFPHMRLEY	VSTETFTNELINRPS	AR-DRMTEFRERYR-	196
E.coli	FVEGKSNQLARAAAR	QVADNPGGAYNPLFL	YGGTGLGKTHLLHAV	GNGIMARKPNAKVY	MHSERFVQDMVK--A	LQNNAIIEFKRYR-	227
T.mar.	FVVGPGNSFAYHAAL	EVAKHPGR-YNPLFI	YGGVGLGKTHLLQSI	GNVYVQNEPDLRVMY	ITSEKFLNDLVD--S	MKEGKLENEFREYR	193
H.pyl.	FVVGSCNNTVYEIAK	KVAQSDTPPYNPVLF	YGGTGLGKTHILNAI	GNHALEK--HKKVVL	VTSEDFLTDFLK--H	LDNKTMDSFKAKYR-	203
P.mar.	AADLILVDDIQFIEG	KEYTQEEFFHTFNAL	HDAGSQIVLASDRPP	SQIPRLQERLMSRFS	MGLIADVQAPDLETR	MAILQKKAHERVGL	307
Syn.sp.	SADFLILDDIQFIK	KEYTQEEFFHTFNSL	HEAGQVQVVASDRAP	QRIPGLQDRLLSRFS	MGLIADIQVPDLETR	MAILQKKAEDRIRL	292
B.sut.	NVDVLLIDDIQFLAG	KEQTQEEFFHTFNTL	HEESKQIVISSDRPP	KEIPTLEDRLRSRFE	WGLITDITPPDLETR	IAILRKKAKAEGLDI	296
M.tub.	DVDVLLVDDIQFIEG	KEGIQEEFFHTFNTL	HNANKQIVISSDRPP	KQLATLEDRLRTRFE	WGLITDVQPELETR	IAILRKKAQMERLAV	353
T.th.	SVDLLLVDDVQFIAG	KERTQEEFFHTFNAL	YEAHKQIILSSDRPP	KDILTLLEARLSRFE	WGLITDNPAPDLETR	IAILKMNAS-SGPED	285
E.coli	SVDALLIDDIQFFAN	KERSQEEFFHTFNAL	LEGNQOIILTSDRYP	KEINGVEDRLKSRFG	WGLTVAIEPPELETR	VAILMKKADENDIRL	317
T.mar.	KVDILLIDDVQFLIG	KTGVQTELFTFNEL	HDSGKQIVICSDREP	QKLSEFQDRLVSRFQ	MGLVAKLEPPDEETR	KSIARKMLEIEHGEL	283
H.pyl.	HCDFLLDDAQFLQG	KPKLEEEFFHTFNEL	HANSKQIVLISDRSP	KNIAGLEDRLKSRFE	WGITAKVMPPDLETK	LSIVKQKCOLNQITL	293
P.mar.	PRDLIQFIAGRFTSN	IRELEGALTRAIFA	SITGLPMTVDSIAPM	LD----PNGQGEVET	PKQVLDKVAEVFKVT	PDEMRSASRRR-PVS	392
Syn.sp.	PKEVIEYIASHYTSN	IRELEGALIRAIAYT	SLSNVAMTVENIAPV	LN----PPVEKVAAA	PETIITIVAQHYQLK	VEELLSNSRRR-EVS	377
B.sut.	PNEVMYLIANQIDSN	IRELEGALIRVVAYS	SLINKDINADLAAEA	LKDII-PSSKPKVIT	IKEIQRVVGQQFNK	LEDFAKAKRTK-SVA	384
M.tub.	PDDVLELIASSIERN	IRELEGALIRVTAF	SLNKTPIDKALAEIV	LRDLI-ADANTMQIS	AATIMAATAEYFDTT	VEELRGPGKTR-ALA	441
T.th.	PEDALEYIARQVTSN	IREWEGALMRASPFA	SLNGVELTRAVAACA	LRHLR-P--RELEAD	PLEIRKAGPVRPE	TPGGAHGERRKKEVV	372
E.coli	PGEVAFPIAKRLRSN	VRELEGALNRVIANA	NFTGRAITIDFVREA	LRDLL-A-LQEKLV	IDNIQKTVAEYYKIK	VADLLSKRRSR-SVA	404
T.mar.	PEEVLNFVAENVDDN	LRRLRGAI IKLLVYK	ETTGKEVDLKEAILL	LKDFIKPNRVKAMP	IDELIEIVAKVTGVP	REEILSNSRNV-KAL	372
H.pyl.	PEEVMEYIAQHISDN	IRQMEGAI IKISVNA	NLMNASIDLNLAKTV	LEDL--QKDHAEGSS	LENILLAVAQSLNLK	SSEIKVSSRQK-NVA	380
P.mar.	QARQVGMVLMRQGTN	LSLPRIGDTFGGKDH	TTVMYAIEQVEKKLS	S-----DPQIA	SQVQKIRDLLQIDSR	RKR----	461
Syn.sp.	LARQVGMVLMRQHTD	LSLPRIGEAFGGKDH	TTVMYSCDKITQLQQ	K-----DWETS	QTLTSLSHRINIAGQ	APES----	447
B.sut.	FPRQIAMYLSREMTD	SSLPKIGEEFGGRDH	TTVIHAHEKISKLLA	D-----DEQLQ	QHVKEIKEQLK----	-----	446
M.tub.	QSRQIAMYLCRELTD	LSLPKIGQAFG-RDH	TTVMYAQRKILSEMA	E-----RREVF	DHVKELTTRIRQRSK	R-----	507
T.th.	LPRQLAMYLVLRELTP	ASLPEIGQLFGGRDH	TTVRYAIQKVQELAG	KP-----DREVQ	GLLRTLREACTDPVD	NLWITCG	446
E.coli	RPRQMAMALAKELTN	HSLPEIGDAFGGRDH	TTVLHACRKIEQLRE	E-----SHDIK	EDFSNLIRTLSS----	-----	467
T.mar.	TARRIGMYVAKNYLK	SSLRTIAEFKN-RSH	PVVVDVSKVKVDSLL	KG-----NKQLK	ALIDEVIGEISRRAL	SG-----	440
H.pyl.	LARKLVVYFARLYTP	NPTLSLAQFLDLKDH	SSISKMYSGVKMLE	EESKPFVLSLREEIK	NRLNELNDKKTAFNS	SE-----	457

Figure 19

A)

GTGTGCGACGAGGCCGTCTGGCAACACGTTCTGGAGCACA
 TCCGCCGACGATCACCGAGGTGGAGTTCCACACCTGGTT
 TGAAAGGATCCGCCCTTGGGGATCCGGGACGGGGTGCTG 120
 GAGCTCGCCGTGCCACCTCCTTTGCCCTGGACTGGATCC
 GCGGCCACTACGCCGCCTCATCCAGGAGGGCCCTCGGCT
 CCTCGGGGCCAGGCGCCCCGGTTTGGAGCTCCGGGTGGTG 240
 CCGGGGTTCGTAGTCCAGGAGGACATCTTCCAGCCCCCGC
 CGAGCCCCCGGCCAAGCTCAACCCGAAGATAACCTTTAA
 AACTTCGTGGTGGGGCCCAACAACATCCATGGCCCCACGGC 360
 GCGCCGTGGCCGTGGCCGAGTCCCCCGGCCGGGCCTACA
 ACCCCCTCTTCATCTACGGGGGCCGTGGCCTGGGAAAGAC
 CTACCTGATGCACGCCGTGGGCCCCACTCCGTGCGAAGCGC 480
 TTCCCCCACATGAGATTAGAGTACGTTTCCACGGAAACTT
 TCACCAACGAGCTCATCAACCGGCCATCCGCGAGGGACCG
 GATGACGGAGTTCCGGGAGCGGTACCGCTCCGTGGACCTC 600
 CTGCTGGTGGACGACGTCCAGTTCATCGCCGGAAGGAGC
 GCACCCAGGAGGAGTTTTTCCACACCTTCAACGCCCTTTA
 CGAGGCCCACAAGCAGATCATCTCTCCTCCGACCGGCCG 720
 CCCAAGGACATCTCACCTGGAGGCGCGCTGCGGAGCC
 GCTTTGAGTGGGGCCTGATCACCGACAATCCAGCCCCCGA
 CCTGGAACCCGGATCGCCATCTGAAGATGAACGCCAGC 840
 AGCGGGCCTGAGGATCCCGAGGACGCCCTGGAGTACATCG
 CCGGCAGGTACCTCCAACATCCGGGAGTGGGAAGGGGC
 CCTCATGCGGGCATCGCCTTTCGCCTCCCTCAACGGCGTT 960
 GAGCTGACCCGCGCCGTGGCGGCCAAGGCTCTCCGACATC
 TTCGCCCCAGGGAGCTGGAGGCGGACCCCTTGGAGATCAT
 CCGCAAAGCGGCGGGACCAAGTTCGGCCTGAAACCCCGGGA 1080
 GGAGCTCACGGGAGCGCCGAAGAAGGAGGTGGTCTCTCC
 CCGGCAGCTCGCCATGTACCTGGTGGCGGAGCTCACCCC
 GGCCTCCCTGCCCGAGATCGACCAGCTCAACGACGACCGG 1200
 GACCACACCACGGTCTCTACGCCATCCAGAAGGTCCAGG
 AGCTCGCGGAAAGCGACCGGGAGGTGCAGGGCCTCCTCCG
 CACCTCCGGGAGGCGTGCACATGA

B)

VSHEAVWQHVLHRRSITEVEFHTWFERIRPLGIRDGVL
 ELAVPTSFALDWIRRHAGLIQEGPRLPGAQAPRFELRVV
 PGVVVQEDIFQPPSPPAQAQPEDTFKTSWWGPTTPWPHG 120
 GAVAVAESPGRAYNPLFIYGGRLGKTYLMHAVGPLRAKR
 FPHMRLEYVSTETFTNELINRPSARDRMTEFRERYRSVDL
 LLVDDVQFIAGKERTQEEFFHTFNALYEAHKQIILSSDRP 240
 PKDILTLEARLRSRFEWGLITDNPAPDLETRIAILKMNAS
 SGPEDPEDALEYIARQVTSNIREWEGALMRASPFASLNGV
 ELTRAVALALRHLRPRELEADPLEIRKAAGPVRPETPG 360
 GAHGERRKKEVVLPRQLAMYLVRCLTPASLPEIDQLNDDR
 DHTTVLYAIQKVQELAESDREVQGLLRTLREACT

Figure 20

A)

ATGAACATAACGGTTCCCAAAAACTCCTCTCGGACCAGC 40
 TTTCCCTCCTGGAGCGCATCGTCCCCTCTAGAAGCGCCAA
 CCCCCTCTACACCTACCTGGGGCTTTACGCCGAGGAAGGG 120
 GCCTTGATCCTCTTCGGGACCAACGGGGAGGTGGACCTCG
 AGGTCCGCCTCCCCGCCGAGGCCCAAAGCCTTCCCCGGGT 200
 GCTCGTCCCCGCCAGCCCTTCTTCCAGCTGGTGGGAGC
 CTTCTGGGGACCTCGTGGCCCTCGGCCTCGCCTCGGAGC 280
 CGGGCCAGGGGGGGCAGCTGGAGCTCTCCTCCGGGCGTTT
 CCGCACCCGGCTCAGCCTGGCCCTGCCGAGGGCTACCCC 360
 GAGCTTCTGGTGGCCGAGGGGGAGGACAAGGGGGCCTTCC
 CCCTCCGGACGCGGATGCCCTCCGGGGAGCTCGTCAAGGC 440
 CTTGACCCACGTGCGCTACGCCGCGAGCAACGAGGAGTAC
 CGGGCCATCTTCCGCGGGGTGCAGCTGGAGTTCTCCCCC 520
 AGGGCTTCCGGGCGGTGGCCTCCGACGGGTACCGCCTCGC
 CCTCTAGACCTGCCCCTGCCCAAGGGTTCCAGGCCAAG 600
 GCCGTGGTCCCCGCCCGGAGCGTGGACGAGATGGTGGGG
 TCCTGAAGGGGGCGGACGGGGCCGAGGCCGTCTCGCCCT 680
 GGGCGAGGGGGTGTGGCCCTGGCCCTCGAGGGCGGAAGC
 GGGGTCCGGATGGCCCTCCGCCTCATGGAAGGGGAGTTCC 760
 CCGACTACCAGAGGGTCATCCCCCAGGAGTTCCGCCCTCAA
 GGTCCAGGTGGAGGGGGAGGCCCTCAGGGAGGCGGTGCGC 840
 CGGGTGAGCGTCCTCTCCGACCGGCAGAACACCGGGTGG
 ACCTCCTTTTGGAGGAAGGCCGGATCCTCCTCTCCGCCGA 920
 GGGGGACTACGGCAAGGGGCAGGAGGAGGTGCCCGCCCAG
 GTGGAGGGGCCGGACATGGCCGTGGCCTACAACGCCCGCT 1000
 ACCTCCTCGAGGCCCTCGCCCCGTGGGGGACCGGGCCCA
 CCTGGGCATCTCCGGGCCCCACGAGCCCCGAGCCTCATCTGG 1080
 GGGGACGGGGAGGGGTACCGGGCGGTGGTGGTGGCCCTCA
 GGGTCTAG 1128

B)

MNITVPKLLSDQLSLLERIVPSRSANPLYTYLGLYAEAG 40
 ALILFGTNGEVDLEVRPAEAQSLPRVLVPAQPFQLVRS
 LPGDLVALGLASEPGGGQLELSSGRFRTRLSLAPAEYYP 120
 ELLVPEGEDKGAFPLRTRMPSELVKALTHVRYAASNEEY
 RAIFRGVQLEFSPQGFRAVASDGYRLALYDLPLPQGFQAK 200
 AVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALEGGS
 GVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVR 280
 RVSVLSDRQNHRVDLLLEGRILLSAEGDYKGQEEVPAQ
 VEGPDMAYAYNARYLLEALAPVGDRAHLGISGPTSPSLIW 360
 GDGEGYRAVVVPLRVZ

Figure 21

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

MNITVPKKLLSDQSLSLRIVTPSRANPLYTYLGLYAEEGALILFGTNGEVDLEVRPAEY
MKFTVEREHLKPLQVQVSGPLGGRTPLPILGNLLQVADGTLSTGTDLMEMVARVALV
MKFIIEREQLLKLQVQVSGPLGGRTPLPILGNLLKVTENTLSTGTDLMEMMARVSL
MQFSISRENLLKLQVQVSGVLSNRNPVILNNVLQIEDYRLTITGTDLLEVELSSQTQLS
MHFTIQREALLKLQVLVAGVRRQTLPVLSNVLVQVQQLSTGTDLLEVELVGRVQLE
MKFTIQNDILTQNLKKITRVLVKNISFPILNLIQVEDGTLSTTTNLEIELISKIEII
* *

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

AQSLP-RVLVPAQPFFQLVRSPLPGDLVALGLASEPGQGQLELSSGRFTRRLSLAPAEY
QPHEPGATTVPARKFFDICRGLP-EGAEIAVQLE---GERMLVSRGRSRFSLSTLPAADF
QSHEIGATTVPARKFFDIWRGLP-EGAEISVELD---GDRLLVSRGRSRFSLSTLPASDF
SSSENGTFTIPAKKFLDICRTLS-DDSEITVTFE---QDRALVQSGRSRFTLATQPAEY
EPAEPGEITVPARKLMDICKSLP-NDALIDIKVD---EQKLLVKGARSRFTLSTLPANDF
TKYIPGKTTISGRKILNICRTLS-EKSIKMQLK---NKKMYISSENSNYILSTLSADTF
* *

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

PELLVPEGEDKGAFPLRTRMPSPGELVKALTHVRYAASNEEYRAIFRGVQLEFSPQGFRAV
PNLDD---WQSEVEFTLPQAT---MKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTV
PNLDD---WQSEVEFTLPQAT---LKRLIESTQFSMAHQDVRYYLNGMLFETENTEELRTV
PNLTD---WQSEVDFELPQNT---LRRLIEATQFSMANQDARYFLNGMKFETEGNLLRTV
PTVEE---GPGSLTCNLEQSK---LRRLIERTSFAMAQQDVRYYLNGMLLEVSRNLTIRAV
PNHQN---FDYISKFDISSNI---LKEMIEKTEFSMGKQDVRYYLNGMLLEKKDKKFLRSV
* *

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

ASDGYRLALYDLPLPQGFQA--KAVVPARSVDEMVRVLKGADGAEAVLALGEGVLALALE
ATDGHRLAVCSMPIGQSLPS-HSVIVPRKGVIELMRMLDG-GDNPLRVQIGSNNIRAHVG
ATDGHRLAAMDIGQSLPG-HSVIVPRKGVIELMRMLDGSSESLQLQIGSNNIRAHVG
ATDGHRLAVCTISLEQELQN-HSVILPRKGVLELVRLLT-NDEPARLQIGTNNLRVHLK
STDGHRLALC SMSAPIEQEDRHQVIVPRKGILELARLLTD-PEGMVSIVLQGHHIRATGT
ATDGYRLAISYTLQKKDINF-FSIIIPNKAVMELLKLLNT-QPQLLNILIGSNSIRIYTK
..** ***. *

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

GGSGVRMALRLMEGEFPDYQRVI PQEFALKVQVEGEALREAVRRVSVLSDRQNHRVDLL
---DFIFTSKLVDGRFPDYRRVL PKNPKHLEAGCDLLKQAFARAAILSNEKFRGVRLYV
---DFIFTSKLVDGRFPDYRRVL PKNPTKTIVAGCDILKQAFSRAAILSNEKFRGVRLINL
---NIVFTSKLIDGRFPDYRRVL PRNATKIVEGNWEMLKQAFARASILSNERARSVRLSL
---EFTFTSKLVDGKFPDYERVLPKGGDKLVVGDRQALREAFSRTAILSNEKYRGIRLQL
---NLIFTTQLIEGEVPDYKSVL FKEKKNP IITNSILLKSLLRVAILAHEKFCGIEIKI
* *

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

EEGRILLSAEGDYGK-QQEEVPAQVEGPDMAVAYNARYLLEALAPVG-DRAHLGISGPTS
SENQLKITANNPEQEEAAEILDVITYSGAEMEIGFNVSYVLDVLNALKCENVRMMLTDSVS
TNGQLKITANNPEQEEAAEIVDVQYQGEEMEIGFNVSYLLDVLNLTLC EEVKLLLTDAVS
KENQLKITASNTHEEAAEIVDVNYNGEELEVGFNVITYILDVLNALKCNQVRMCLTDAFS
AAGQLKIQANNPEQEEAAEISVDYEGSSLEIGFNVSYLLDVLGVMTQVRLILSDSNS
ENGKFKVLSDNQEEETAEDLFEIDYFGEKIEISINVYLLDVINNIKSENIALFLNKS
* *

T. th. beta
E. coli. bet
P. mirab. be
H. infl. bet
P. put. beta
B. cap. beta

PSLIWGDG-EGYRAVVVPLRVZ (ID#108)
SVQIEDAASQSAAYVMPMRLZ (ID#109)
SVQENVASAAAAYVMPMRL- (ID#110)
SCLIENCESSCEYVIMPMRL- (ID#111)
SALLQEAGNDDSSYVMPMRL- (ID#112)
SIOIEAENSSNAYVMMLLKR- (ID#113)

Figure 22

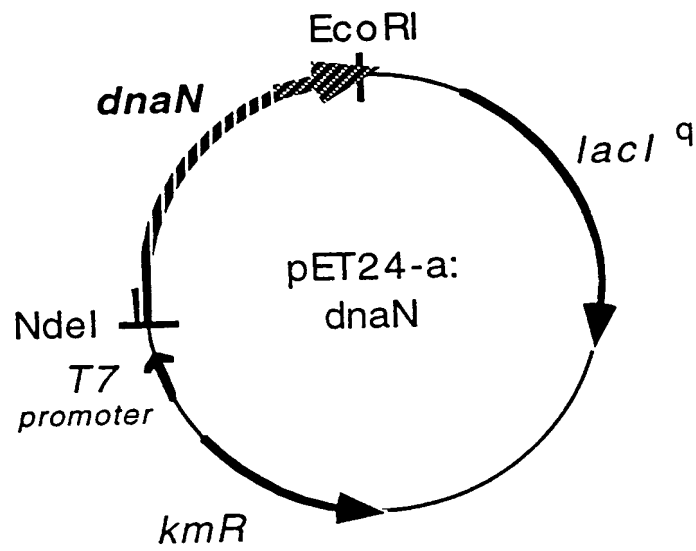
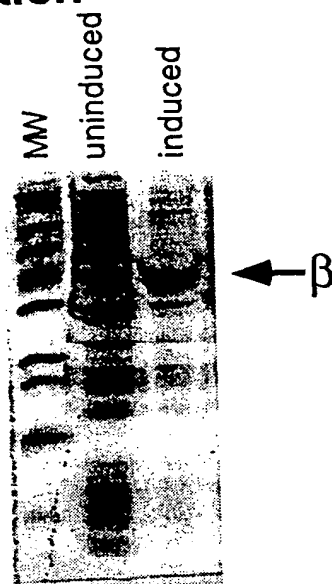


Figure 23

A) Induction

↓
Lysis
↓
Heat Step
↓

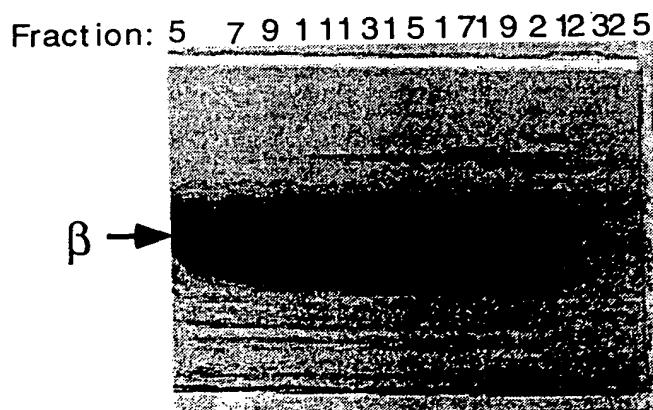
B) MonoQ Column

Figure 24

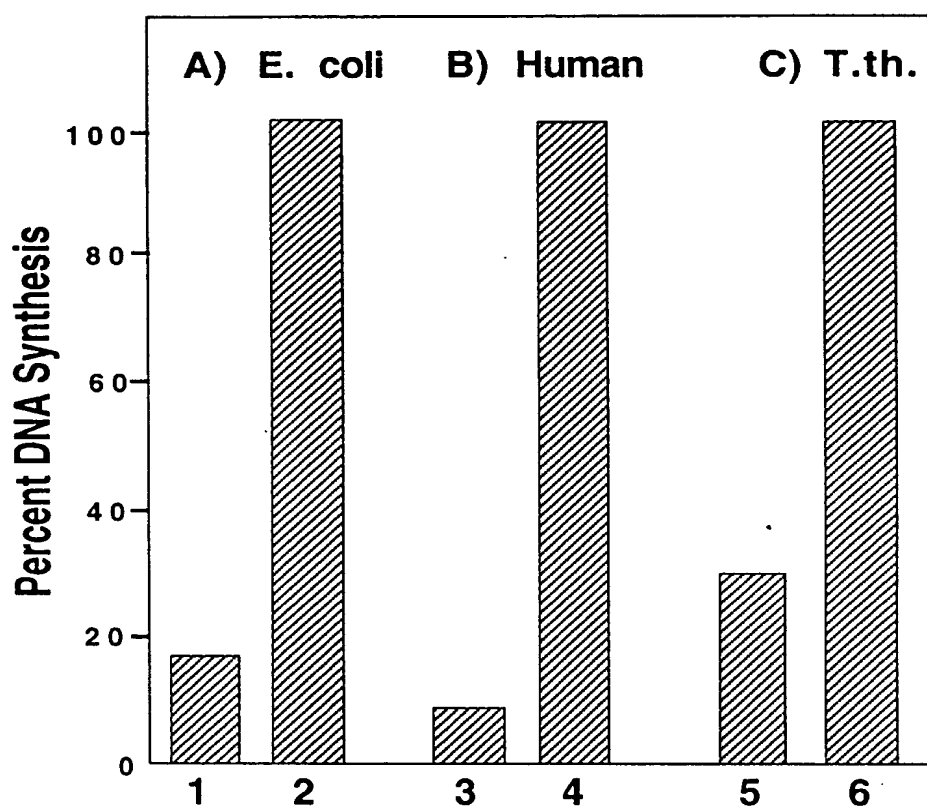
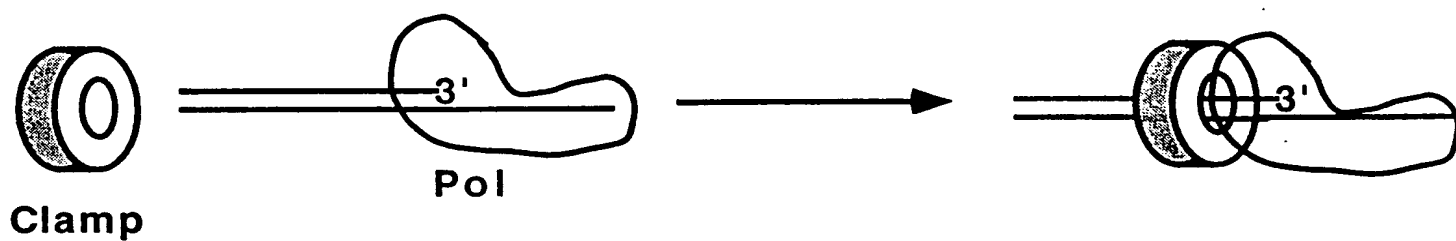


Figure 25

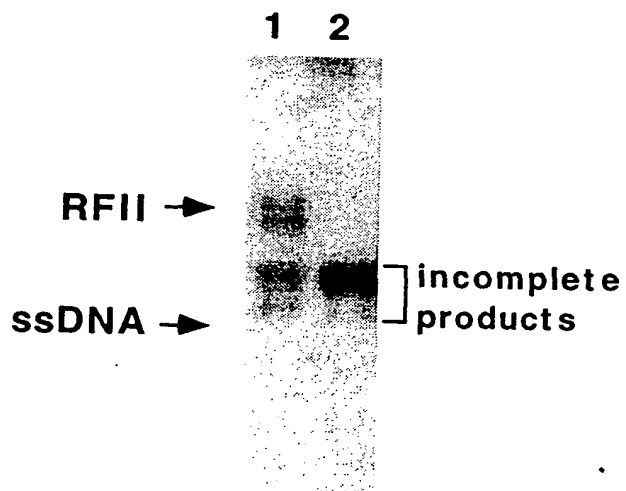
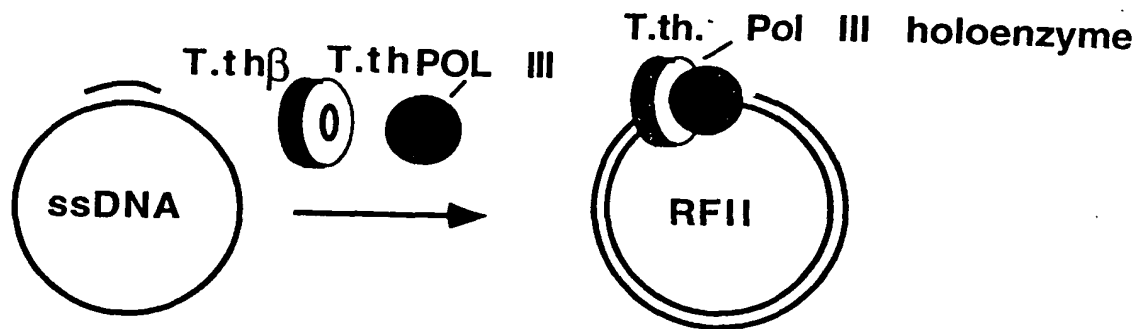


Figure 26